

Package ‘easyEWAS’

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Title Perform and visualize EWAS analysis

Version 1.0.0

Description easyEWAS is an R package designed for conducting Epigenome-Wide Association Study (EWAS) and visualizing results. Users only need to provide sample data, and methylation values to easily perform EWAS analysis. The package supports two statistical methods, linear models and linear mixed-effects models. It utilizes the CMplot package to generate visualizations, including Manhattan plots and QQ plots, based on EWAS results. Additionally, the use of parallel computing significantly improves computational efficiency, making it suitable for researchers less experienced in EWAS or parallel computing.

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Encoding UTF-8

Roxxygen list(markdown = TRUE)

RoxxygenNote 7.3.1

Imports boot, boot.pval, CMplot, ddpcr, doParallel, dplyr, foreach, lmerTest, magrittr, parallel, pbapply, stringr, survival, tictoc, vroom

Suggests knitr, rmarkdown

VignetteBuilder knitr

Depends R (>= 4.0.0)

LazyData true

NeedsCompilation no

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R topics documented:

bootEWAS	2
initEwas	3
loadEwas	3
plotEwas	4
transType	5
zeroEwas	5

Index

7

bootEWAS*Perform Bootstrap Validation***Description**

Users can perform internal validation of the selected methylation sites based on the bootstrap method.

Usage

```
bootEWAS(input, filterP = "PVAL", threshold = 0.05, CpGs = NULL, times = 100,
seed = 123, file.name = "default")
```

Arguments

<code>input</code>	An R6 class object integrating all information.
<code>filterP</code>	The p value column name, including PVAL, FDR, and Bonfferoni. Users use this P-value to screen for significance sites and do internal verification.
<code>threshold</code>	num. Used to filter the P-value to determine the threshold of significance sites. The default is 0.05.
<code>CpGs</code>	chr. The name of the methylation site specified by the user for bootstrap analysis, separated by commas. Be careful not to have Spaces. such as "cpg1,cpg2".
<code>times</code>	Number of bootstrap times specified by the user. The default value is 100 times.
<code>seed</code>	The number of seeds used to ensure repeatable results when bootstrap resamples.
<code>file.name</code>	User-defined name of the bootstrap result file. If the default is automatically named "bootresult".

Value

An R6 class object integrating all information.

Examples

```
## Not run:
res <- initEwas(outpath = "default")
res <- loadEwas(input = res, ExpoData = "default", MethyData = "default")
res <- transType(input = res, Vars = "cov1", TypeTo = "factor")
res <- zeroEwas(input = res, chipType = "EPICV2", model = "lm", expo = "default", adjustP = TRUE)
res <- plotEwas(input = res, pval = "PVAL", file.name = "zero")
res <- bootEWAS(input = res, filterP = "PVAL", threshold = 0.05, times = 100, seed = 123)

## End(Not run)
```

initEwas	<i>Initialize the EWAS module</i>
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Description

It can generate an R6 class object integrating all information.

Usage

```
initEwas(outpath = "default")
```

Arguments

outpath	The default is the current working path, or it can be user-defined. A folder named "result_easyEWAS" will be generated in this path to store the EWAS analysis results.
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Value

input, An R6 class object integrating all information.

Examples

```
## Not run:  
res <- initEwas(outpath = "default")  
  
## End(Not run)
```

loadEwas	<i>Load all data files for EWAS</i>
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Description

Upload sample data and methylation data for EWAS

Usage

```
loadEwas(input, Expopath = NULL, Methypath = NULL, ExpoData = "default",  
MethyData = "default")
```

Arguments

input	An R6 class object integrating all information.
Expopath	Path for storing the user sample data. Each row of the sample data repinputents an individual, and each column repinputents exposed variables, covariates, and other information. The first column must be the sample name. If default, load the example data.
Methypath	Path to store user methylation data. Each row of methylation data repinputents a methylation site, and each column repinputents an individual with methylation values, such as beta and M values. The first column must be the methylation site name. If default, load the example data.

ExpoData	The data.frame of the user-supplied sample data that has been loaded into the R environment. If default, the example data inside the package is used. The first column must be the sample name.
MethyData	The data.frame of the user-supplied methylation data that has been loaded into the R environment. If default, an example of methylation data inside the package is loaded. The first column must be the methylation site name.

Value

input, An R6 class object integrating all information.

Examples

```
## Not run:
res <- initEwas(outpath = "default")
res <- loadEwas(input = res, ExpoData = "default", MethyData = "default")

## End(Not run)
```

plotEwas

Visualizing the results of EWAS analysis

Description

Visualize EWAS results based on the CMplot package, including Manhattan plots, QQ plots, etc. Optional parameters are the same as those in the CMplot function.

Usage

```
plotEwas(input, pval = "PVAL", ...)
```

Arguments

input	An R6 class object integrating all information.
pval	The user needs to specify the name of the p value selected for the result visualization. Applicable when exposed as a categorical variable.

Value

input, An R6 class object integrating all information.

Examples

```
## Not run:
res <- initEwas(outpath = "default")
res <- loadEwas(input = res, ExpoData = "default", MethyData = "default")
res <- transType(input = res, Vars = "cov1", TypeTo = "factor")
res <- zeroEwas(input = res, chipType = "EPICV2", model = "lm", expo = "default", adjustP = TRUE)
res <- plotEwas(input = res, pval = "PVAL", file.name = "zero")

## End(Not run)
```

transType	<i>Convert variable type of sample data</i>
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Description

Transform the variable types of sample data to the desired types as specified by the user.

Usage

```
transType(input, Vars, TypeTo)
```

Arguments

Vars	Variable names that the user wants to convert types for, with each variable name separated by a comma. Ensure there are no spaces.
TypeTo	Data types that the function allows conversion of, including numeric and factor.

Value

input, An R6 class object integrating all information.

Examples

```
## Not run:
res <- initEwas(outpath = "default")
res <- loadEwas(input = res, ExpoData = "default", MethyData = "default")
res <- transType(input = res, Vars = "cov1", TypeTo = "factor")

## End(Not run)
```

zeroEwas	<i>Perform EWAS Analysis</i>
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Description

Perform EWAS analysis to obtain the coefficient value, standard deviation and significance p value (or adjust p value) of each site.

Usage

```
zeroEwas(input, file.name ="default", model = "lm", expo = "default",
cov = NULL,random = NULL, adjustP = TRUE, num_cores = "default")
```

Arguments

input	An R6 class object integrating all information.
file.name	User-customized CSV file name for storing EWAS results. If "default" is chosen, it will be named as "ewasresult".
chipType	The Illumina chip versions for user measurement of methylation data, including "450K ", "EPICV1" and "EPICV2". The default is "EPICV2". Note: The latest Infinium Methylation Screening Array Manifest Files (270K) has also been added, which users can specify using "270K".
model	chr. Statistical model used for EWAS analysis. Options include "lm" and "lmer," with the default set to "lm".
expo	chr. Name of the independent variable used in the EWAS analysis. The default is an exposure variable for the example data.
cov	chr. Name(s) of covariate(s) used in the EWAS analysis.
time	When the user selects the Cox proportional risk model, the name of the time variable needs to be specified
status	When the user selects the Cox proportional Risk model, the name of the status variable needs to be specified
random	When selecting the "lmer" model, provide the names of the random effects to be added.
adjustP	logical. Whether to calculate adjusted p-values(FDR). The default is set to TRUE.
num_cores	num. Number of cores to use during parallel computation. If set to "default," it will be configured to the maximum available cores minus one.

Value

input, An R6 class object integrating all information.

Examples

```
## Not run:
res <- initEwas(outpath = "default")
res <- loadEwas(input = res, ExpoData = "default", MethyData = "default")
res <- transType(input = res, Vars = "cov1", TypeTo = "factor")
res <- zeroEwas(input = res, file.name = "default", chipType = "EPICV2", model = "lm",
expo = "default", adjustP = TRUE, num_cores = "default")

## End(Not run)
```

Index

bootEWAS, 2

initEwas, 3

loadEwas, 3

plotEwas, 4

transType, 5

zeroEwas, 5